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FIG. 1

atgttagccaacagctcctcaaccaacagttctgtttctcccggtgtcctgactaccgacct
accacccgctgcacttggtggtctacagcttggtgctggctgccgggctccccctcaac
gcgctagccctctgggtcttcctgcgcgcgctgcgcgtgcaactcgggtggtgagcgtgtac
atgtgtaacctggcggccagcgacctgctcttcacctctcgcgtgcccggttcgtctctcc
tactacgcactgcaccactggcccttccccgacctcctgtgccagacgacgggcgccatc
ttccagatgaacatgtacggcagctgcatcttcctgatgctcatcaacgtggaccgctac
gccgccatcgtgcacccgctgcgactgcgccacctgcggcggccccgcgtggcgcggtg
ctctgcctgggcgtgtgggcgctcatcctggtggttgccgtgcccgccgcccgcgtgcac
aggccctcgcgttgccgctaccgggacctcgaggtgcgcctatgcttcgagagcttcagc
gacgagctgtggaaaggcaggctgctgccccctcgtgctgctggccgaggcgctgggcttc
ctgctgccccctggcggcggtggtctactcgtcgggccgagtcctctggacgctggcgcg
cccgacgccacgcagagccagcggcggcggaagaccgtgcgcctcctgctggctaacctc
gtcatcttcctgctgtgcttcgtgccctacaacagcacgctggcggtctacgggctgctg
cggagcaagctggtggcgccagcgctgcctgcccgcatcgctgcgcggggtgctgatg
gtgatggtgctgctggcgccgccaactgcgtgctggaccgctggtgtactactttagc
gccgagggcttcgcgaacacctgcgcggcctgggcactccgcaccggggccaggacctcg
gccaccaacgggacgcgggcggcgctcgcgcaatccgaaaggctccgccgtcaccaccgac
gccaccaggccggatgccgccagtcaggggctgctccgacctccgactcccactctctg
tcttccttcacacagtgtccccaggattccgcctctga

FIG. 2

MLANSSSTNSSVLPCPDYRPTHRLHLVVYSLVLAAGLPLNALALWVFLRALRVHSVVS
MCNLAASDLLFTLSLPVRLSYALHHWPFDPDLLCQTTGAI FQMNMYGSCIFLMLINVD
AAIVHPLRLRLHRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCFES
DELWKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLARPDATQSQRRRKTVRLLAN
VIFLLCFVPYNSTLAVYGLLRSLVAASVPARDRVRGVLMMVLLAGANCVLDPLVYYFS
AEGFRNTLRGLGTPHRARTSATNGTRAALAQSERSAVTTDATRPDAASQGLLRPSDSH
SSFTQCPQDSAL

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FIG. 3A

gcgtccgaaaaaaaaaagaaattcctttacatactacaacatgaatagatcttggaacat
tatgctaagtgaataaaccagacacaaaaggacaaatattgtatgattccactcatatg
aggtatctagaataggcaaattcattgagacagaaagtagactagaaccagaagctgaat
ggggtgcggtgggtagtactgcttaatgactgcagagttgttgcttggttgatgaaaaag
ttctatcttctggaaacagagagtggtgacggttaagcaacactgtcttggtcttttttgt
tgttggttggttggtttttgagacggactctcactctgtctcccaggccggagtgcgatggat
tagacctgctaggggagcacttggcaaaactcaaccacagggccttcccctgcctagca
agactgtgctgtcaaatttattcacatgtggctctggtcaagactagcatgcaatcagcc
tatgagggcattattatattattattcccatttttacagatgaagaaactgagaagtcaaa
ccattaagctgaaccacagtttgctttgaccacaaatccagccctcacaggcgcagtgatg
catgtgatgcgtgaaggctgggatgttggtctgtatttgggagttttggttgcttggttg
ttgtctgacatggagtctcactctgtcaccaggctggagtgagtgccgtgatctcggc
tcactgcaacctccgcctcccgggttcaaggactctcctgctgcagcctcccatgtactc
aaagagtttgacctttattctttggataatgaggagctagcctagcacctgggtccaagga
ggtgctccataagaccacctattgatttggtgcttattatctgtctccctccaatggaatg
taaaggaggtgggggcaaagactttttgctttggttccctgctgtgaacatgcctggaact
ttctatgagctcagtaagcaaggaaagaaggaaggaagagatcttgagatagtaacagca
acctaaagcgttttacacacgtcatcttaatctccaaacctcatgaattctctctctct
ctctcattttttgagacagagctctcgctctgtcaccaggctggagtgagtgccgtgat
ctcgactcattgcaacctctgcctcctggattcaatcaattctcatgccttagcctactg
aggagctgggattacaagtgcacgccaccatacccggttaattctttgtatttttagtaga
ggcaagattttgtcatgttggtccagggttggtcttcaactcctggcctcaagtaatccacc
cacatcagcctcccaaagtgtgagatcacaggcatgaggtaccatgcagccgccttttt
tttttttttgagatggagtctcgttttgttacccaggctggagggcagtggtacgatgt
cagctcactgcaacctccgcctcctgggttcaagtgattctcctgtgtgagcctcctgag
tagctgggactacaggtgatgccaccacatctggctaattttttgtatttttagtagaga
cagggttttgcccagggtggccaggctgatctcgaactcctgacctcaggtgatctgccc
cctcagctctcccaaagtgtggattacaggtgtgggcccactacgccggccctggccctct
ttctttcttttttgagatgggctcactctgtcaccaggcaggagtgagtggtgggctt
gaggctcactgcactgcagcctccacctccctggagtcagtgattctctcacctcagcc
tcacaagtagctgggactacgggcatgtgccacaatgcctggctaatttttttaattttt
aatattttttattttatttttttttgagacagagctcttgctctgtcaccaggccggagt
gcaatgggtgtgatctcggtcactgcaacctctgtcgaagcaattctccctgccttagcc
tctgagtagctgggattacaggcgcctgccaccacgcccggctaattttttttttttt
tagtagagacaggattttgccatgttggtccaggatgggtctcaacctcctgacctcaggtg
atccgcccacctcagcctcccaaagtgtcggattacagatgtgagccaccacgcccagc
cttattttttattttttattttattttattttatttttgagatggagtttactcttgt
tgcccaggctggagtgcaatggcgcgatcttggtcactgcaaaactccacccccagggt
caagcaattctcctgtctcagccccctgagtagctgggattacaggcgcccgccccatg
ccaggctaatttttggtatttttttttagtagagatggggtttcaccatgttggtcaagct
ggtctcgaactcctgacctcaggtgatccacctgcctcggcctcccaaagtgtgggatt
acaggcgtgagccaccgcgcctggctattttttattttttgagacagagtttacttttgt
tgtccaggctggagtgcaatggcacagtctcagctcactgcaacctctgcctcctgggtt
caagcgattctcctgtctcagcctcccgagtagctgggattacaggcgtgcaccaccacg
cccagctaatttttggtatttttagtagagatggggtttcaccatattggacagggtgggtc
tcgaactcctgacctcaggtaatccaccgcctcggcctcccaaatgctgggattacag

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FIG. 3B

gtgtgagccactgcacctggccctgtatTTTTTTgtagagatgggggtttcgccgtgttgc
ccaggctggcccccaactcctaggttcaagcaattggtctgccttggcctcccaaagtgc
caggattacaggtgtaagccattgcacccagccaagattaatTTTTTTgaagtcacacaa
ctaggcaagttagcaaaaaccaagatttaaaccctagggcatccgagtccttgccttcaaacc
tggtgttttaacactatactatatagtcctgcccgtaggaacctattctagcccaatggca
gacttgaggctgagaaaagattcagaaggcctgccagtggagctaaacatttgtgtgtgc
agccctgtctctgtataacttccggcttgccttcctattccaggtctctgctgctgatga
agctgtgaccaaacgcacccaacccttggcagccatctgtccctgcagccatagcccaca
ttcccatgacctccctctgcttgttttgggaccatgtctgtacagcctctaggccccagc
cccggaggtgaatgccatgccatgattctggtgtgctccatggcatccccagcctagctc
ccaatcccactttggcacg

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FIG. 4

ACACACATGCCATTGCGCTGTCCGTGCCCCACTCCCAACGCCTCTCGTTCTGGGAGGCTT
 ACAGGGTGTACACACAAGAAGGTGGGCTGGGCACTTGGACCTTTGGGTGGCAATTCCAGC
 TTAGCAACGCAGAAGAGTACAAAGTGTGGAAGCCAGGGCCCAGGGAAGGCAGTGCTGCTG
 GAAATGGCTTCTTTAAACTGTGAGCACGCAGAGCACCCCTTCTCCAGCGGTGGGAAGTGA
 TGCAGAGAGCCCCACCCGTGCAGAGGGCAGAAGAGGACGAAATGCCTTTGGGTGGGCAGGG
 CATTAAACTGCTAAAAGCTGGTTAGATGGAACAGAAAAATGGGCATTCTGGATCTAAACCG
 CCACAGGGGCCTGAGAGCTGAAGAGCACCAGGTTTGGTGGACAAAGCTACTGAGATGCCT
 GTTCATCTGCTGACTTCTGTCTAGGCTCATGGATGCCACCCCTTTTCATTTTCGGCCTAGG
 CTTCCCCTGCTCACCCTGAGGCCTAATAACAAGAGTTCTATGGACAGAACTACATTCTT
 TCTCGCATAGTGACTTGTGACAATTTAGACTTGGCATCCAGCATGGGATAGTTGGGGCAA
 GGCAAACTAACTTAGAGTTTCCCCCTCAACAACATCCAAGTCAAACCCCTTTTGGTT
 ATCCTTTCTTCCATCACATCCCCCTTTCCAGGCCTCCTCCATTTTAGGTCTTAATATTC
 TTTCTTTTTCTCTCTCTCTCGTTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CTCTCTCTCTCCCTCTCTCCTTTGTCCAGAGTAAGGATAAAATTCTTTCTACTAAAGCAC
 TGGTTCTCAAACCTTTTGGTCTCAGACCCCACTCTTAGAAATTGAGGATCTCAAAGAGCT
 TTGCTTATATTTTGTCTTTTGATACTTACCATACTAGAAATTAAAGCGAATACATTTTT
 AAAATAAATACACATGCACACATTACATTAGCCATGGGAGCAATAATGTCACCACACACA
 CTTTCATGAAGCCTCTGGAAAACCTCTACAGTATACTTGTGAGAGAATGAGAGTGAAAGGGA
 CAAATAACATCTGTGTAGCAGTATTATGAAAATAGCTTGACCTCGTGGACTTCCTCAGAG
 GGTGGTCCCTGGATCACACTTTGAGAACCATACTTGTCTCTGAAGTATTGGAGTTCATGT
 CTAACCTCTTCCCAGGGCATTATGTACAGTGCTTTTTTATTACTGTGGGGAGAGGGCAGTG
 CTAATAAATTAATCACTACTGATAAAAAAAAAAAAAAAAAAAG

FIG. 5

MLANSSSTNS	SVLPCPDYRP	THRLHLVVYS	<u>LVLAAGLPLN</u>	<u>ALALWVFLRA</u>
LRVHSVSVSY	<u>MCNLAASDLL</u>	<u>FTLSLPVRLS</u>	<u>YYALHHWPFP</u>	<u>DLLCQTTGAI</u>
<u>FQNMNYGSCI</u>	<u>FLMLINVDRY</u>	AAIVHPLRLR	HLRRPRVARL	<u>LCLGVWALIL</u>
<u>VFAVPAARVH</u>	RPSRCRYRDL	EVRLCFESFS	DELWKGRLLP	<u>LVLLAEALGF</u>
<u>LLPLAAVVYS</u>	<u>SGRVFWTLAR</u>	PDATQSQRRR	KTVRLLLANL	<u>VIFLLCFVPY</u>
<u>NSTLAVYGLL</u>	RSKLVAASVP	<u>ARDRVRGVLM</u>	<u>VMVLLAGANC</u>	<u>VLDPLVYYFS</u>
AEGFRNTLRG	LGTPHRARTS	ATNGTRAALA	QSERSAVTTD	ATRPDAASQG
LLRPSDSHSL	SSFTQCPQDS	AL		

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FIG. 6A

```

GP68_HUMAN      ~~~~~~MGNITADNSSMSCTIDHTIHOTLA
O46685          ~~~~~~MGNITADNTSMNCDIDHTIHOTLA
O15132          ~~~~~~MGDRRFIDFQFQDSNSSLRPRLGNATANNTCTIVD.DSFK..YNLN
P2Y9_HUMAN      ~~~~~~MGDRRFIDFQFQDSNSSLRPRLGNATANNTCTIVD.DSFK..YNLN
P2Y5_CHICK      ~~~~~~MVSSNCSTE.DSFK..YTLY
P2Y5_HUMAN      ~~~~~~MVSVNSSHCFYN.DSFK..YTLY
HGPRBMY3        ~~~~~~MLANSSSTNSSVLPCPDYRPTHRLH
GPRH_HUMAN      ~~~~~~MNGLEVAPPGLITNF..SLATAE.QCGQET.PLENMLF
O35811          ~~~~~~MTSAESLLFTSLGPSPSSGDGDCRFNE.EFKFILL
SSR4_HUMAN      MSAPSTLPPGGEEGLGTAWPSAANASSAPAEAEAVAGPGDARAAGMVAI

GP68_HUMAN      PVVYVTVLVVGFNPANCLSLYFGYLOIKARNELGVYLCNLTVADLFYTCSL
O46685          PVVYVTVLVVGFNPANCLSLYFGYLOIKARNELGVYLCNLTVADLFYTCSL
O15132          GAVYSVVFILGLITNSVSLFVFCFRMKMRSETAIFTNLAVSDLLFVCTL
P2Y9_HUMAN      GAVYSVVFILGLITNSVSLFVFCFRMKMRSETAIFTNLAVSDLLFVCTL
P2Y5_CHICK      GCVFSSMVFVLGLIANCVAIYIFTFTLKVRNETTTTYMLNLASDLLFVFTL
P2Y5_HUMAN      GCMFSSMVFVLGLVSNCAVYIFICVLKVRNETTTTYMINLAMS DLLFVFTL
HGPRBMY3        LVVYSILVLAAGLPLNALALWVFLRALRVHSVVSVMCNLAASDLLFTLSL
GPRH_HUMAN      ASFYLLIDFILA LGNTLALWLFIRDHKS GTPANVFILMHLAVADLSCVLVL
O35811          PMSYAVVEVLGLALNAPTLLWLFLFRLRPWDAATATYMFHLASDTLYVLSL
SSR4_HUMAN      QCTYALVCEVGLVGNALVTFVILRYAKMKTATNTYLLNLAVADELFMLSV

GP68_HUMAN      PEWLOY.VLQHDNWSHGDLSCQVCGILLYENIYISVGFLCCISVDRYLAV
O46685          PEWLOY.VLQHDHWSHDDLSCQVCGILLYENIYISVGFLCCISVDRYLAV
O15132          PEKTFYNF..NRHWPFPGDTLCKISGTAFLTNIYGSMLFELTCISVDRFLAI
P2Y9_HUMAN      PEKTFYNF..NRHWPFPGDTLCKISGTAFLTNIYGSMLFELTCISVDRFLAI
P2Y5_CHICK      PERTFYFV..VRNWPFPGDVLCISVTLFYTNMYGSILFELTCISVDRFLAI
P2Y5_HUMAN      PERTFYFT..TRNWPFPGDLLCKISVMLFYTNMYGSILFELTCISVDRFLAI
HGPRBMY3        EVRLSYA..LHHWPFPDLLCQTIGATFQNMNYGSCIFMLINVDRYAAI
GPRH_HUMAN      PTERLVYHFSG.NHWPFGETACRLTGFLFYLNMYASTYFELTCISADRFELAI
O35811          PT.LVYYAARNHWPFPGTGLCKFVRFLFYWNLYCSVLFTLCISVHRYLGI
SSR4_HUMAN      PE..VASSAALRHWPFGSVLCRAVLSVDGLNMFTSVFCLTVLSVDRYVAV

GP68_HUMAN      AHPFRFHQERTLKAAGVGSVVIWAKEL...LTSIYFLMH EEVIEDENQHR
O46685          AHPFRFHQERTLKAAMGVSALIWVKEL...LTSIYFLMH EEVVEDADRHR
O15132          VYPFRSRTIRTRNSAIVCAGVWILVLSGGTSASLFS..TTNV..NNATT
P2Y9_HUMAN      VYPFRSRTIRTRNSAIVCAGVWILVLSGGTSASLFS..TTNV..NNATT
P2Y5_CHICK      VHPFRSKTLRTKRNARIVCAVWITVLAGSTPASFEQ..STNRQNNTEQR
P2Y5_HUMAN      VYPEKSKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQ..STHSQGNNA SE
HGPRBMY3        VHELRLRLRLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVR
GPRH_HUMAN      VHPVKS LKLRRPLYAHLACAFLW.VVAVAMAPLLVSPQTV...QTNHTV
O35811          CHELRAIRWGRPRFASLLCLGVWL.VVAGCLVPNLFFVTIN...ANGTTI
SSR4_HUMAN      VHELRAATYRRPSVAKLINLGVWLASLLVTLPIATEFA..DTRPARGGQAV

GP68_HUMAN      VCFEHYPIQAWQR...AINYYRFLVGFLFPICLLIASYQGILRAVRRSHG
O46685          VCFEHYPLEPRQR...GINYYRFLVGFLFPICLLIASYRGILRAVRRSHG
O15132          TCFEGLSKRVWKTYLSKITIFIEVVGFIPLILNVSCSSVVLRTL RKP.A
P2Y9_HUMAN      TCFEGESKRVWKTYLSKITIFIEVVGFIPLILNVSCSSVVLRTL RKP.A
P2Y5_CHICK      TCFENPESTWKTYLSRIVIFIEIVGFFIPLILNVTCSTMVLR TLNKP.L
P2Y5_HUMAN      ACFENPEATWKTYLSRIVIFIEIVGFFIPLILNVTCSSMVLKTLTKP.V
HGPRBMY3        LCFESESDLEWKGRLLPPIVLAELGELLPLAAVYSSGRVFWTLARPD A
GPRH_HUMAN      VCLQ.LYREKASHHAL.MSLAV...AFTFPFITTVTCYLLIIRSLROGL.
O35811          LCHDTTLPEEFDHVY.FSSAMVLLFGLPFLITLVCYGLMARRLYRPLP
SSR4_HUMAN      ACNLQWHPAWS...AVFVVYTFLLGFLLPVLAIGLCYLLIVGKRAVAL

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FIG. 6B

```

GP68_HUMAN      TQ....KSRKDOTQRLVLSTVVIFLACFLPYHVLL....LVRSVWEASC
O46685          TQ....KSRKDOTQRLVLSTVVIFLACFLPYHVLL....LVRSLWESSC
O15132          TLS..QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFELYALVRSQAITNC
P2Y9_HUMAN      TLS..QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFELYALVRSQAITNC
P2Y5_CHICK      TLS..RNKLSKKKVLKMI FVHLVIFCFCFVPYNITLILYSLMRTQTWINC
P2Y5_HUMAN      TLS..RSKINKTKVLKMI FVHLIIFCFCFVPYNINLILYSLVRTQTFVNC
HGPRBMY3        TQS..Q...RRRKTVRITLANLVIFLLCFVPYNSTLAVYGLRSKLVAAS
GPRH_HUMAN      .RV..EKRL..KTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHGASC
O35811          GAG..QSSS..RLRSLRTIAVVLTVFAVCFVPEHITRTTY.YQARLLQADC
SSR4_HUMAN      RAGWQRRRSEKKITRELVLMVVVVFVLCWMPFYVQQLNLVVTSLDAT..

GP68_HUMAN      DFAKGVEN.AYHFSLLLTSENCVADPVLVYCFVSETHRDLARI RGACLAF
O46685          DFAKGIFN.AYHFSLLLTSENCVADPVLVYCFVSETHRDLARI RGACLAF
O15132          FLER.FAKIMYPITLCLATLNCCFDPIYYFTLESFOKSFYI.NAHIRME
P2Y9_HUMAN      FLER.FAKIMYPITLCLATLNCCFDPIYYFTLESFOKSFYI.NAHIRME
P2Y5_CHICK      SMVT.AVRTMYPVTLCTAVSNCCFDPIVYYFTSDT..NSELDKKQVHQN
P2Y5_HUMAN      SMVA.AVRTMYPITLCTAVSNCCFDPIVYYFTSDTIONSIKMKNWSVRRS
HGPRBMY3        VPARDRVRGVLMVMVLLAGANCVLDPLVYYFSAEGFRNTLRGLGTPHRAR
GPRH_HUMAN      ATQRI..LALANRITSCLTSLNGALDPTMYFFVAEKERHALCNLLCGKRLK
O35811          HVLNI..VNVVYKVTREPLASANSCLDPVLYLFTGDKYRNQLOQLCRGSK..
SSR4_HUMAN      .....VNHSVLIILSYANSCANPILYGFLSDNERRSFORMLC...LR

GP68_HUMAN      LTCSRTGRAREAYPLGAPEASGKSGAQGEPELTKLHPAFQTPNSPGSG
O46685          LTCARTGRAREAYPLGAPEASGKS...EDPEVLTRLHPAFQTPHPPGMG
O15132          SLFKTETPLTTKPSLPAIQEEVSDQTTNNGGELMLESTF~~~~~
P2Y9_HUMAN      SLFKTETPLTTKPSLPAIQEEVSDQTTNNGGELMLESTF~~~~~
P2Y5_CHICK      T~~~~~
P2Y5_HUMAN      DFRFSEVHGAENFIQHNLTLSKIFDNESAA~~~~~
HGPRBMY3        TSATNGTRALALQERSAVTTDATRPDAASQGLIRPSDSHSLSSFTQCPQ
GPRH_HUMAN      GPPPSFEGKTNESSLSAKSEL~~~~~
O35811          .PKP....RTAASSLALVTLHEESISRWADTHQDSTFSAYEGDRL~~~~
SSR4_HUMAN      CCLLEGAGCAEEEPDYYATAALKS...KGGAGCMCPPLPCQQEALQPEPG

GP68_HUMAN      GFPTGRLA~~~~
O46685          GSPAGGLS~~~~
O15132          ~~~~~~
P2Y9_HUMAN      ~~~~~~
P2Y5_CHICK      ~~~~~~
P2Y5_HUMAN      ~~~~~~
HGPRBMY3        DSAL~~~~~
GPRH_HUMAN      ~~~~~~
O35811          ~~~~~~
SSR4_HUMAN      RKRIPLTRTTTF

```

SEQUENCE	SEQ ID NO:
GP68_HUMAN	8
O46685	9
O15132	10
P2Y9_HUMAN	11
P2Y5_CHICK	12
P2Y5_HUMAN	13
HGPRBMY3	2
GPRH_HUMAN	14
O35811	15
SSR4_HUMAN	16

FIG. 7

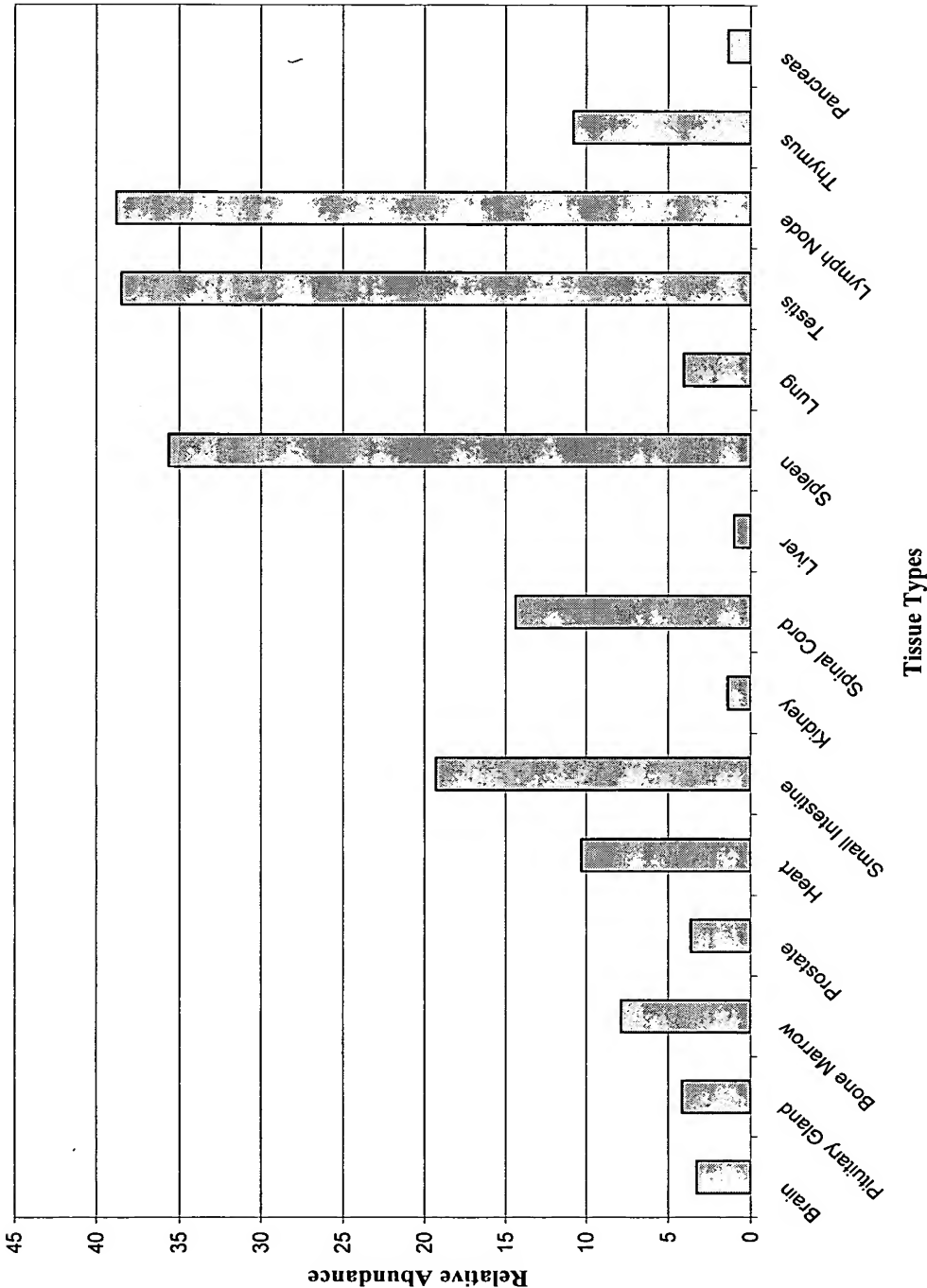
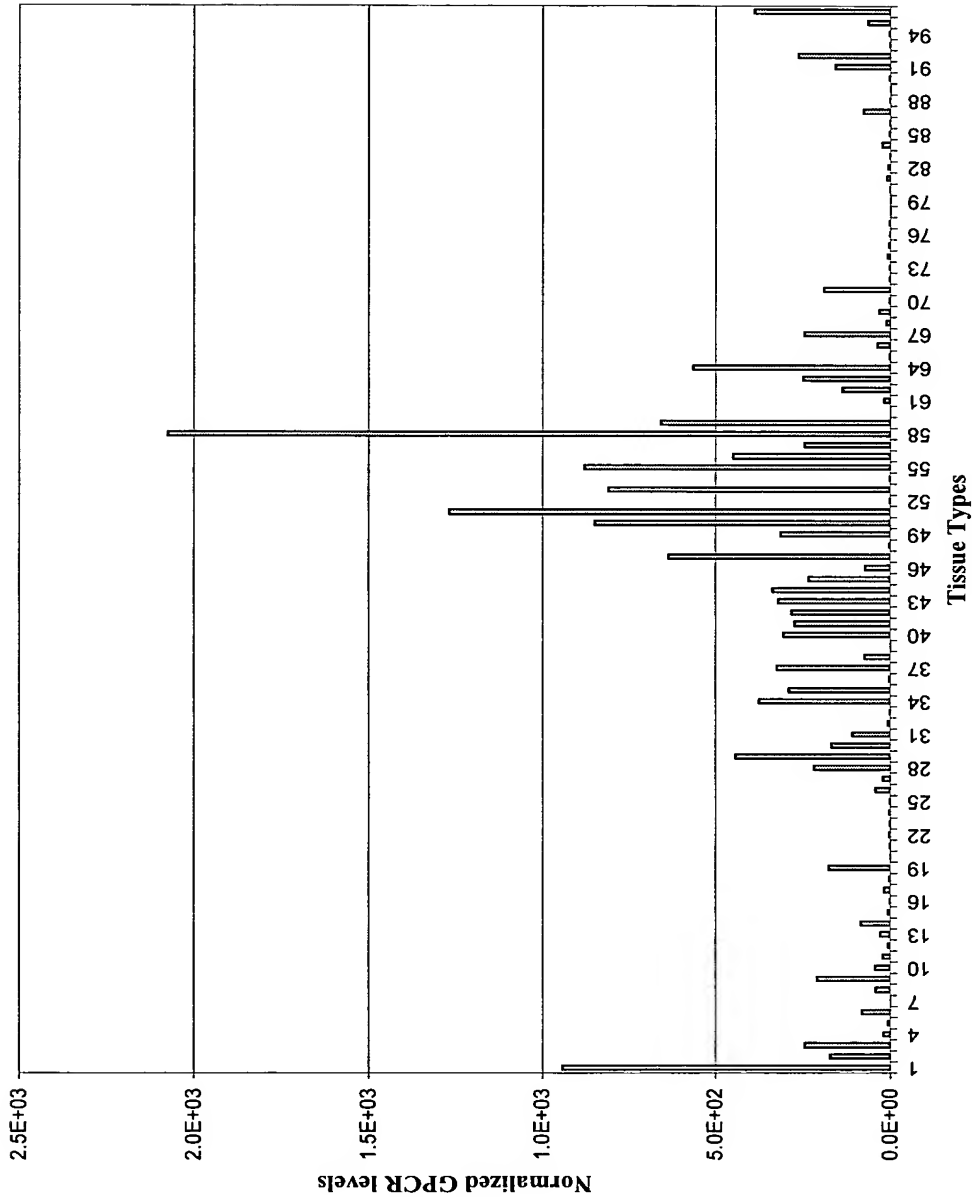


FIG. 8



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FIG. 9

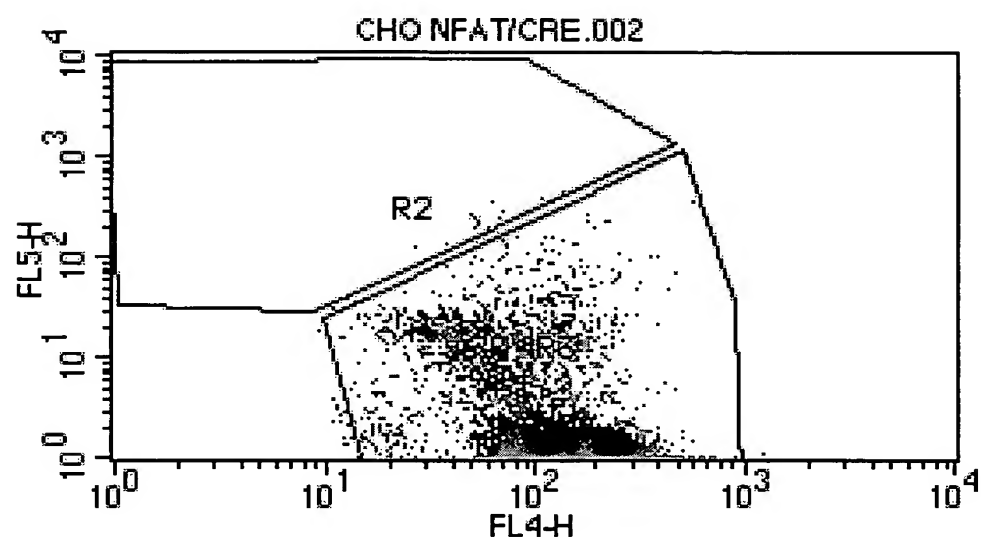
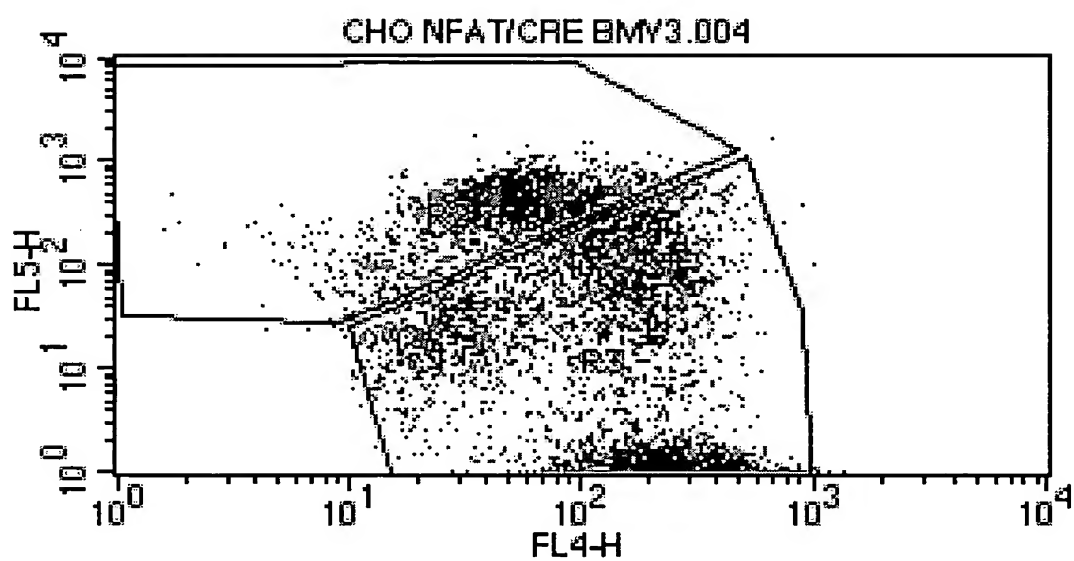


FIG. 10



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FIG. 11

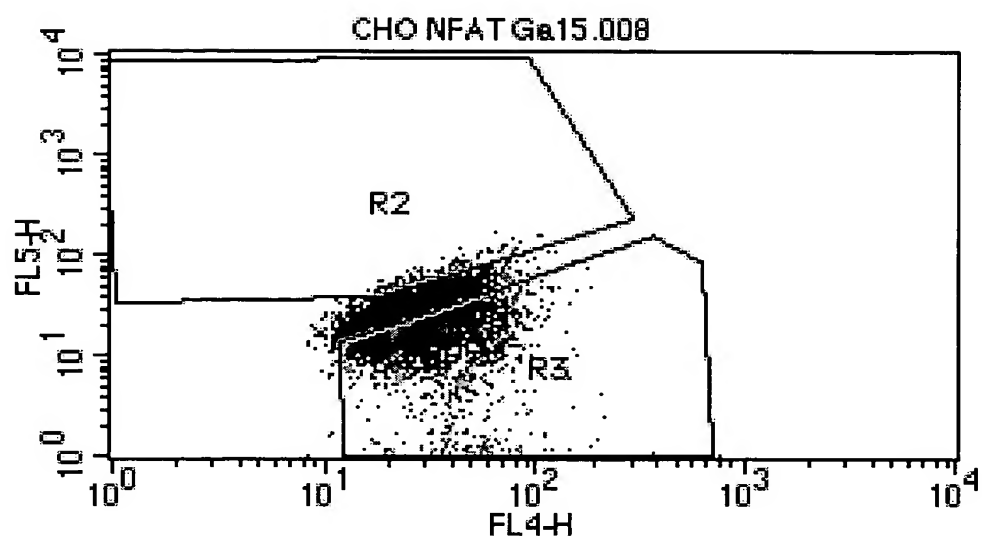
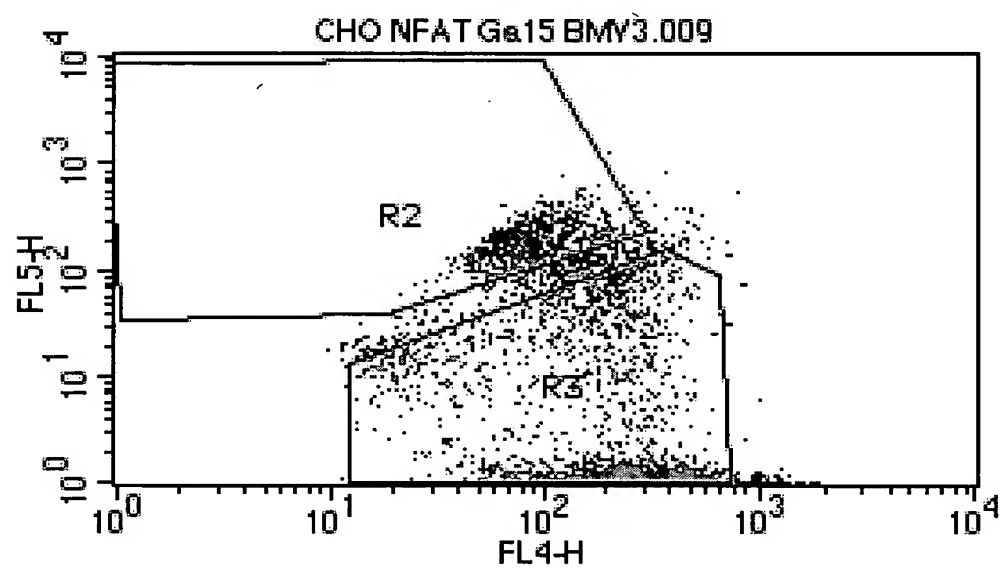


FIG. 12



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FIG. 13A

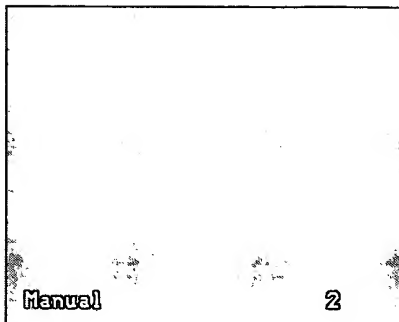


FIG. 13B

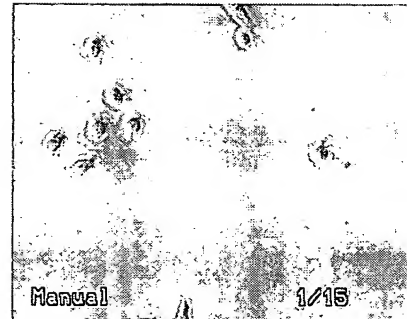


FIG. 13C

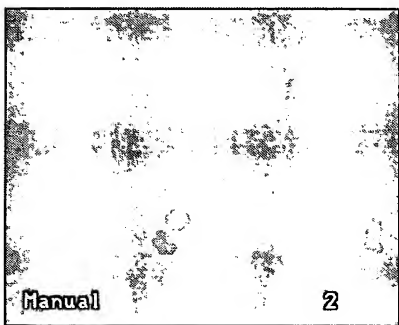
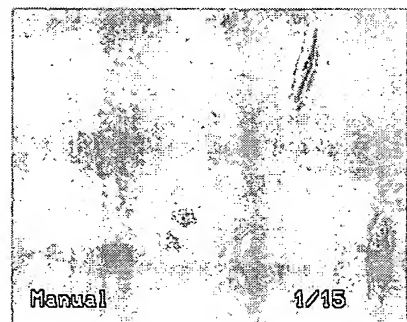


FIG. 13D



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FIG. 14A

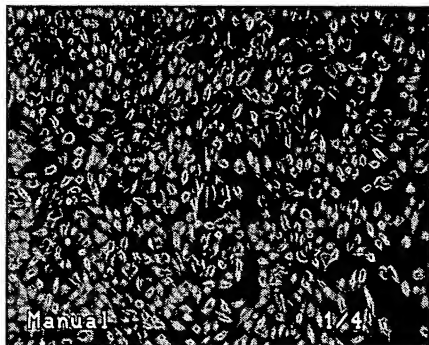


FIG. 14B

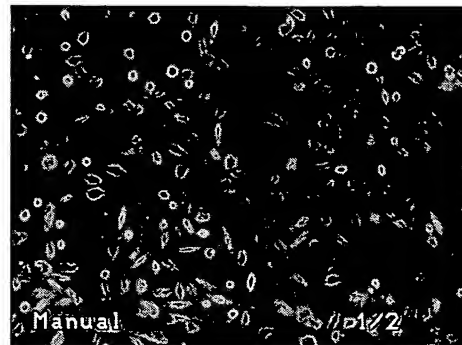


FIG. 14C

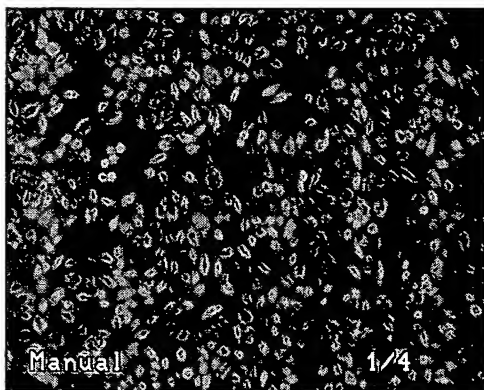
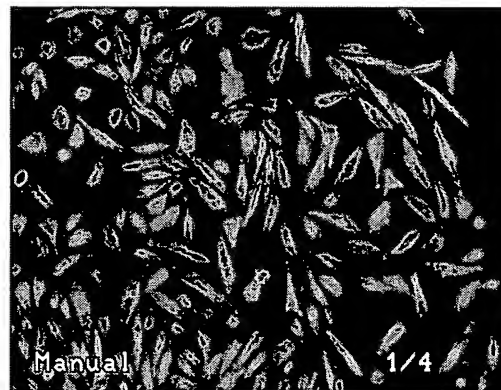


FIG. 14D



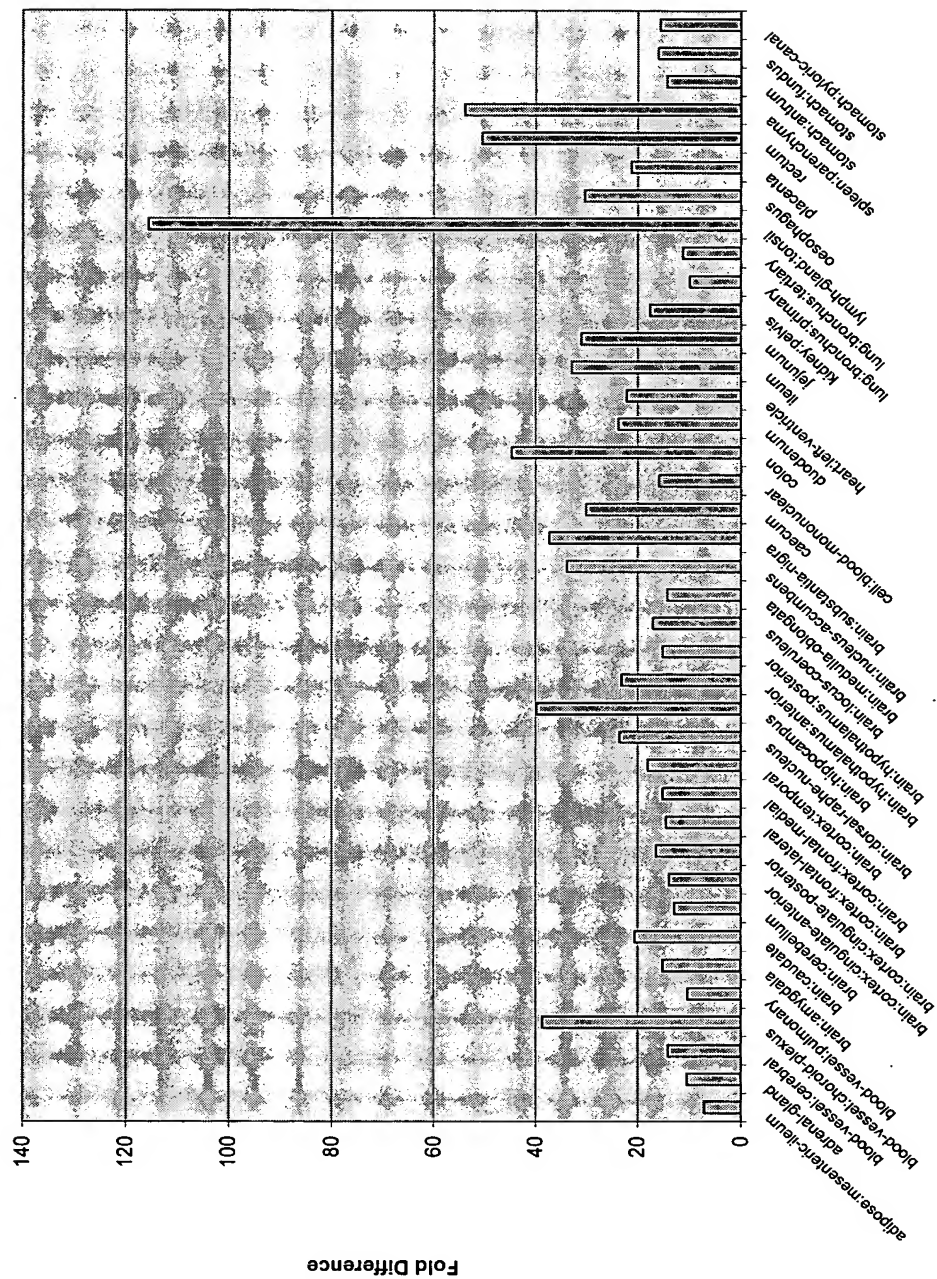
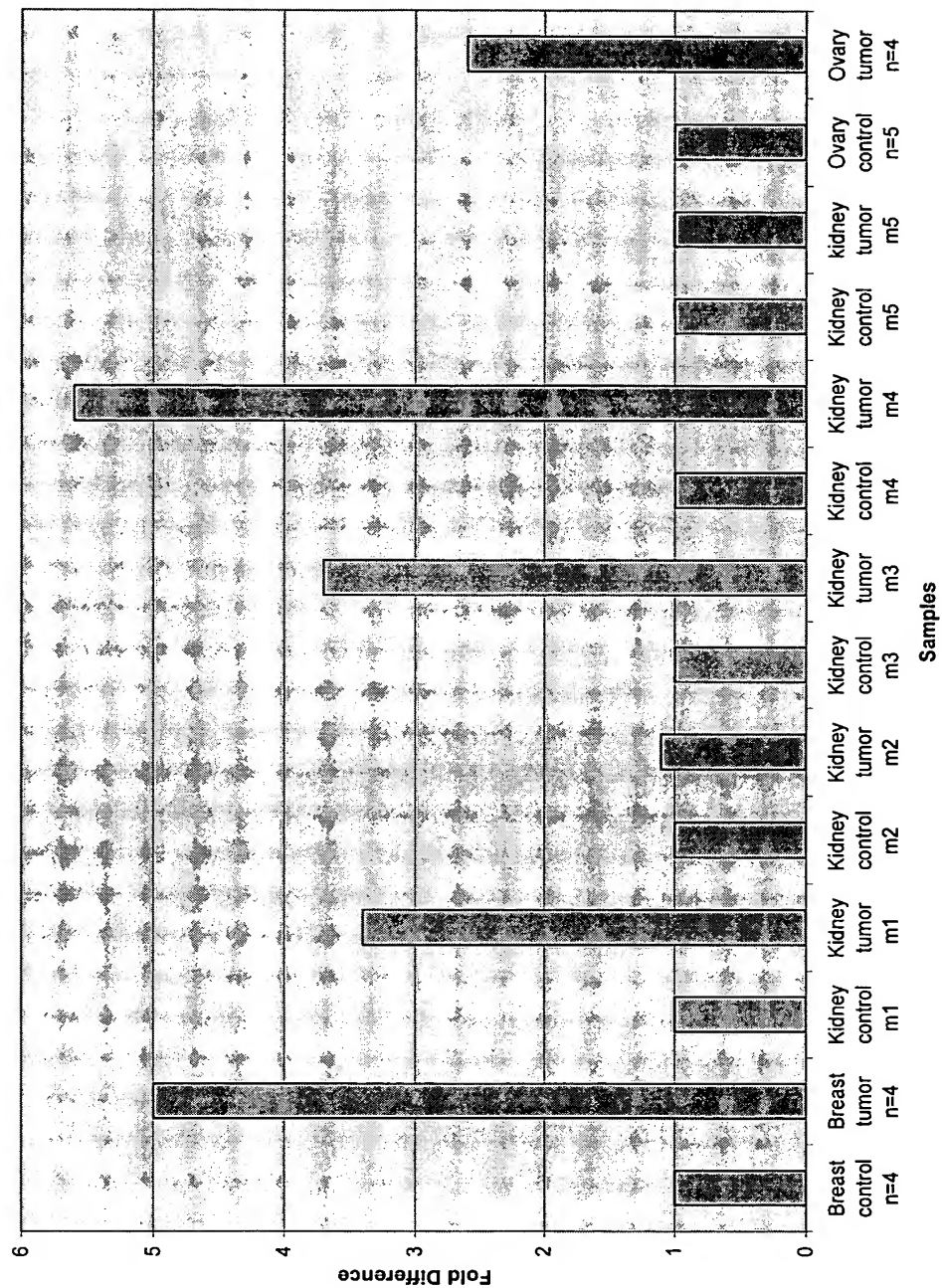
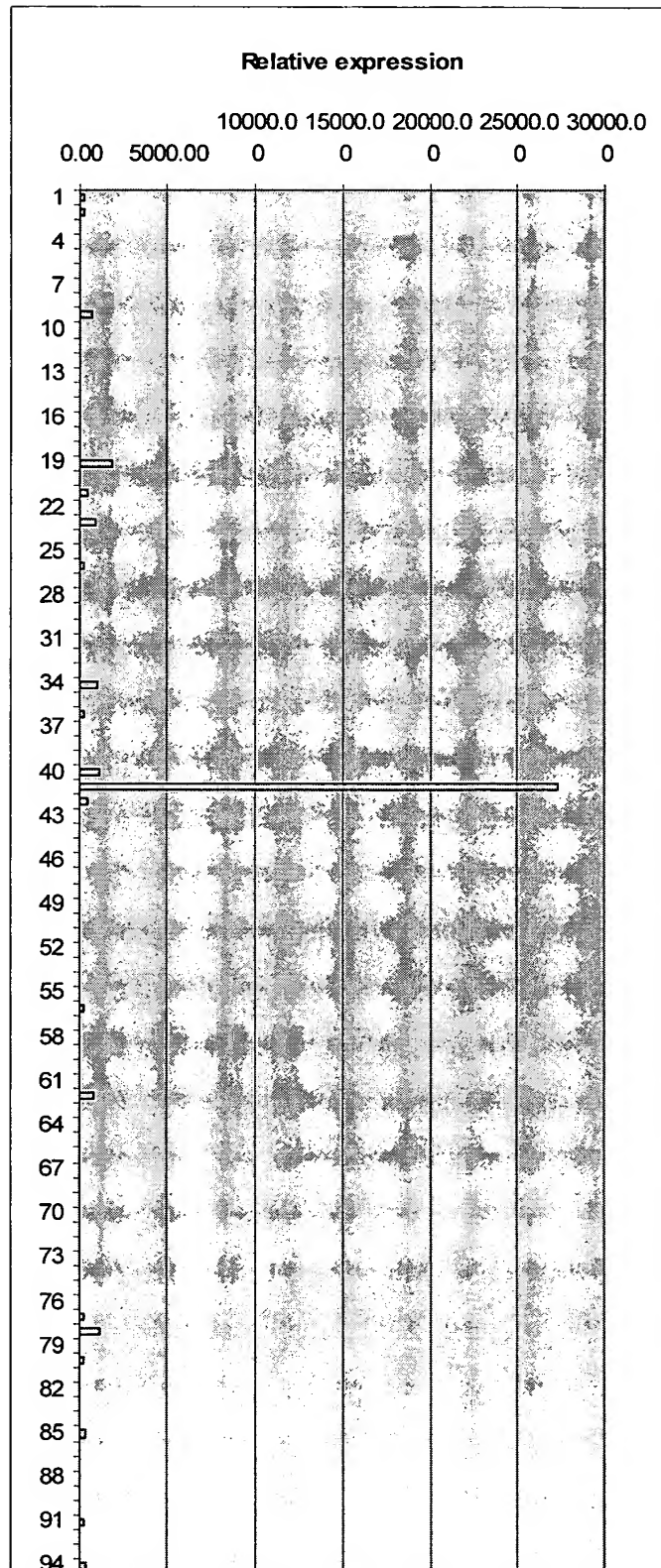


FIG. 16



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FIG. 17



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FIG. 18A

<u>BINDER NO.</u>	<u>SEQUENCE</u>	<u>SEQ ID NO:</u>
1	LEAKIWVVPAPS	17
2	TGQTKIWYPHST	18
3	VYSKVWLLPAGQ	19
4	HLKVWEVRSPGP	20
5	NAKVWTVPSKPP	21
6	KVWIP ^T STWLQT	22
7	KVWSL ^D DISAPQH	23
8	ADVLHATPSEKVWLL	24
9	KVVDSNHKVWLVSQT	25
10	NHDNTKKVW ^I LA	26
11	KLWILADNFTNR	35
12	INSPHELKKLWLLPP	36
13	FPHKLWVLPVKT	37
14	KLWTIPSNDYPP	38
15	KLWELYPTVPAG	39
16	KLWIPHTSQPFL	40
17	KLWDITAPLPKP	41
18	NAKLWQIPAI ^P H	42
19	KLWVPQNRPELV	43
20	KLWELYPTVPAG	44
21	TSTPHRVWQLPV	45
22	TTPHRVWNLPLEAQQ	46

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FIG. 18B

BINDER NO.	SEQUENCE	SEQ ID NO:
1	L E A K I W V V P A P S TTG GAG GCG AAG ATT TGG GTG GTG CCT GCG CCT TCT CTX GAO GCX AAO ATB TGG GTX GTX CCX GCX CCX TCX TTO AGZ	17 47 78
2	T G Q T K I W Y P H S T ACT GGG CAG ACT AAG ATT TGG TAT CCG CAT TCT ACG GCX GGX CAO ACX AAO ATB TGG TAZ CCX CAZ TCX ACX AGZ	18 48 79
3	V Y S K V W L L P A G Q GTT TAT TCG AAG GTT TGG CTG CTT CCG GCG GGT CAG GTX TAZ TCX AAO GTX TGG CTX CTX CCX GCX GGX CAO AGZ CTO CTO	19 49 80
4	H L K V W E V R S P G P CAT CTT AAG GTG TGG GAG GTT CGG TCG CCT GGG CCT CAZ CTX AAO GTX TGG GAO GTX CGX TCX CCX GGX CCX TTO AGO AGZ	20 50 81
5	N A K V W T V P S K P P AAT GCG AAG GTG TGG ACG GTT CCG TCG AAG CCG CCT AAZ GCX AAO GTX TGG ACX GTX CCX TCX AAO CCX CCX AGZ	21 51 82
6	K V W I P T S T W L Q T AAG GTG TGG ATT CCT ACG AGT ACT TGG CTG CAG ACT AAO GTX TGG ATB CCX ACX TCX ACX TGG CTX CAO ACX AGZ TTO	22 52 83
7	K V W S L D I S A P Q H AAG GTT TGG AGT TTG GAT ATT TCG GCT CCG CAG CAT AAO GTX TGG TCX CTX GAZ ATB TCX GCX CCX CAO CAZ AGX TTO AGZ	23 53 84
8	A D V L H A T P S E K V W L L CCG GAT GTG TTG CAT GCA TAC CCC TCT GAG AAG GTC TGG CTT CTG GCX GAZ GTX CTX CAZ GCX ACX CCX TCX GAO AAO GTX TGG CTX CTX TTO AGZ TTO	24 54 85
9	K V V D S N H K V W L V S Q T AAG GTG GTG GAT AGT AAT CAT AAG GTT TGG CTG GTT TCT CAG ACT AAO GTX GTX GAZ TCX AAZ CAZ AAO GTX TGG CTX GTX TCX CAO ACX AGZ TTO AGZ	25 55 86
10	N H D N T K K V W I L A AAT CAT GAT AAT ACT AAG AAG GTT TGG ATT CTG GCT AAZ CAZ GAZ AAZ ACX AAO AAO GTX TGG ATB CTX GCX TTO	26 56 87
11	K L W I L A D N F T N R AAG CTT TGG ATT CTG GCT GAT AAT TTT ACG AAT CGG AAO CTX TGG ATB CTX GCX GAZ AAZ TTZ ACX AAZ CGX TTO TGO	35 57 88

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FIG. 18C

BINDER NO.	SEQUENCE														SEQ ID NO:	
12	I	N	S	P	H	E	L	K	K	L	W	L	L	P	P	36
	ATT	AAT	TCT	CCG	CAT	GAA	CTT	AAG	AAG	CTG	TGG	CTT	CTG	CCG	CCT	57
	ATB	AAZ	<u>TCX</u>	CCX	CAZ	GAO	<u>CTX</u>	AAO	AAO	<u>CTX</u>	TGG	<u>CTX</u>	<u>CTX</u>	CCX	CCX	89
			AGX				TTO			TTO		TTO	TTO			
13	F	P	H	K	L	W	V	L	P	V	K	T				37
	TTT	CCG	CAT	AAG	TTG	TGG	GTT	TTG	CCG	GTG	AAG	ACT				58
	TTZ	CCX	CAZ	AAO	<u>CTX</u>	TGG	GTX	<u>CTX</u>	CCX	GTX	AAO	ACX				90
					TTO			TTO								
14	K	L	W	T	I	P	S	N	D	Y	P	P				38
	AAG	CTG	TGG	ACG	ATT	CCT	AGT	AAT	GAT	TAT	CCG	CCT				59
	AAO	<u>CTX</u>	TGG	ACX	ATB	CCX	<u>TCX</u>	AAZ	GAZ	TAZ	CCX	CCX				91
		TTO					AGZ									
15	K	L	W	E	L	Y	P	T	V	P	A	G				39
	AAG	CTT	TGG	GAG	TTG	TAT	CCG	ACT	GTG	CCG	GCT	GGT				60
	AAO	<u>CTX</u>	TGG	GAO	<u>CTX</u>	TAZ	CCX	ACX	GTX	CCX	GCX	GGX				92
		TTO			TTO											
16	K	L	W	I	P	H	T	S	Q	P	F	L				40
	AAG	CTG	TGG	ATT	CCT	CAT	ACT	TCT	CAG	CCG	TTT	CTT				61
	AAO	<u>CTX</u>	TGG	ATB	CCX	CAZ	ACX	<u>TCX</u>	CAO	CCX	TTZ	<u>CTX</u>				93
		TTO						AGZ				TTO				
17	K	L	W	D	I	T	A	P	L	P	K	P				41
	AAG	TTG	TGG	GAT	ATT	ACG	GCT	CCT	TTG	CCT	AAG	CCT				62
	AAO	<u>CTX</u>	TGG	GAZ	ATB	ACX	GCX	CCX	<u>CTX</u>	CCX	AAO	CCX				94
		TTO							TTO							
18	N	A	K	L	W	Q	I	P	A	I	P	H				42
	AAT	GCG	AAG	CTT	TGG	TAG	ATT	CCT	GCG	ATT	CCG	CAT				63
	AAZ	GCX	AAO	<u>CTX</u>	TGG	CAO	ATB	CCX	GCX	ATB	CCX	CAZ				95
				TTO												
19	K	L	W	V	P	Q	N	R	P	E	L	V				43
	AAG	CTT	TGG	GTT	CCG	CAG	AAT	CGT	CCG	GAG	CTG	GTG				67
	AAO	<u>CTX</u>	TGG	GTX	CCX	CAO	AAZ	<u>CGX</u>	CCX	GAO	<u>CTX</u>	GTX				96
		TTO						AGO			TTO					
20	K	L	W	E	L	Y	P	T	V	P	A	G				44
	AAG	CTT	TGG	GAG	TTG	TAT	CCG	ACT	GTG	CCG	GCT	GGT				68
	AAO	<u>CTX</u>	TGG	GAO	<u>CTX</u>	TAZ	CCX	ACX	GTX	CCX	GCX	GGX				97
		TTO			TTO											
21	T	S	T	P	H	R	V	W	Q	L	P	V				45
	ACT	TCT	ACT	CCT	CAT	AGG	GTT	TGG	CAG	CTG	CCT	GTT				69
	ACX	<u>TCX</u>	ACX	CCX	CAZ	<u>CGX</u>	GTX	TGG	CAO	<u>CTX</u>	CCX	GTX				98
		AGZ				AGO				TTO						
22	T	T	P	H	R	V	W	N	L	P	L	E	A	Q	Q	46
	ACT	ACT	CCT	CAT	CGT	GTA	TGG	AAC	CTG	CCC	CTG	GAG	GCT	CAG	CAG	70
	ACX	ACX	CCX	CAZ	<u>CGX</u>	GTX	TGG	AAZ	<u>CTX</u>	CCX	<u>CTX</u>	GAO	GCX	CAO	CAO	99
					AGO				TTO		TTO					

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FIG. 19A

<u>GPC RECEPTOR</u>	<u>BINDER SEQUENCE</u>	<u>SEQ ID NO:</u>
HGPRBMY11	THGFGHRVWSVPLRS	73
HGPRBMY23	SRVSGAKVWFLSNWS	74
P2Y10	AMNSHKIWMLPH	75
P2Y10	GLKIWSLPPHHG	76
P2Y10	<u>KVWQMAPTTAFS</u>	77

FIG. 19B

<u>GPC RECEPTOR</u>	<u>BINDER SEQUENCE</u>	<u>SEQ ID NO:</u>
HGPRBMY11	T H G F G H R V W S V P L R S ACT CAT GGT TTT GGT CAT CGT GTG TGG AGT GTT CCG TTG CGT TCG ACX CAZ GGX TTZ GGX CAZ <u>CGX</u> GTX TGG <u>TCX</u> GTX CCX <u>CTX</u> <u>CGX</u> <u>TCX</u> AGO AGZ TTO AGO AGZ	73 100 105
HGPRBMY23	S R V S G A K V W F L S N W S AGT AGG GTG TCT GGT GCG AAG GTT TGG TTT TTG AGT AAT TGG TCT <u>TCX</u> <u>CGX</u> GTX <u>TCX</u> GGX GCX AAO GTX TGG TTZ <u>CTX</u> <u>TCX</u> AAZ TGG <u>TCX</u> AGZ AGO AGZ TTO AGZ AGZ	74 101 106
P2Y10	A M N S H K I W M L P H GCT ATG AAT AGT CAT AAG ATT TGG ATG TTG CCG CAT GCX ATG AAZ <u>TCX</u> CAZ AAO ATB TGG ATG <u>CTX</u> CCX CAZ AGZ TTO	75 102 107
P2Y10	G L K I W S L P P H H G GGT CTG AAG ATT TGG AGT TTG CCG CCG CAT CAT GGG GGX <u>CTX</u> AAO ATB TGG <u>TCX</u> <u>CTX</u> CCX CCX CAZ CAZ GGX TTO AGZ TTO	76 103 108
P2Y10	K V W Q M A P T T A F S AAG GTT TGG TAG ATG GCG CCT ACG ACT GCG TTT TCG AAO GTX TGG CAO ATG GCX CCX ACX ACX GCX TTZ <u>TCX</u> AGZ	77 104 109

FIG. 20

HGPRBMY11

MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSYFLTVLSVVRFLAMVHPFRLHVTISIRSAWILCGI IWILI
MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSCICYLLIIRVLLKVEVPESGLRVS
HRKALTTIIITLIIFFLCFLPYHTLRVHLLTWKVGCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
KSALRKGHPQAKTKCVFPVSVWLRKETRV (SEQ ID NO:110)

HGPRBMY23

MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVI STYIFKMRPWKSSTIIMLNL
ACTDLLYLTSPLFLIHYASGENWIFGDFMCKFIRFSHFNL YSSILFLTCSIFRYCVIIHPMSCFSIHKTRCA
VVACAVVWIIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCPLVIVTLCYTTIIHTL
THGLQTDSCCLKQKARRLTILLLLAFYVCFLPFHILRVIRIESRLLSISCS IENQIHEAYIVSRPLAALNTFGNLL
LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP (SEQ ID NO:111)

P2Y10

MANLDKYTETFKMGSNSTSTA EICYCNVTNVKFQYSLYATTYILIFIPGLLANSAALWVLCRFISKKNKAIIFMIN
LSVADLAHVLSLPLRIYYYISHHWPFQRALCLLCFYLYLNMYASICFLT CISLQRCFFLLKPFRARDWKRRYDV
GISA AIWIVGTACLPFPILRSTD LN NNKSCFADLG YKQMN AVALVGMITVAELAGFVIPVIIAWCTWKTTISL
RQPPMAFQGISERQKALRMVFMCAAVFFICFTPYHINFIFYTMVKETIISSCPVVRIALYFHPFCLCLASLCCLL
DPILYYFMASEFRDQLSRHGSSVTRSR LMSKESGSSMIG (SEQ ID NO:112)